

A1 both of which are hereby incorporated herein in their entirety." and insert ✓ - This application is a continuation of U.S. Serial No. 08/752,844, filed November 21, 1996, which is a continuation-in-part of U.S. Serial No. 08/591,196, filed January 16, 1996, which is a continuation-in-part of U.S. Serial No. 08/372,676, filed January 17, 1995, now U.S. Patent No. 5,612,030, all of which are hereby incorporated herein in their entirety.

On page 12 lines 12-23, please amend the specification as follows:

A2 Amongst the 50 database sequences matched most closely to that of the 1A7 heavy chain variable region, none was identical (Figure 3, Panels A and B). The following summarizes the main points deduced from the comparison.

- The closest match was with a heavy chain fragment. There were 2 deletions and 12 substitution differences.
- The closest match with a full length heavy chain variable region had the following features: There were 3 deletions and [17] 16 substitution differences
- 1A7 differed in length from all sequences but one, due to insertions or deletions of 1 to 8 residues about the VDJ junction. For the sequence of equal length, there were [26] 25 substitution differences.
- All other comparisons showed a total of at least [22] 20 insertions, deletions and substitution differences. Differences appeared throughout the variable region.

On page 85 line 4 to page 86 line 5, please amend the specification as follows:

A3 Amongst the 50 database sequences matched most closely to that of the 1A7 heavy chain variable region, none was identical. The following summarizes the main points deduced from the comparison.

- The closest match was with a heavy chain fragment beginning at residue 9 (designation gp|M36221|MUSIGHAEB\_1). There were 6 substitutions between residues 1 and 97 (before the VDJ junction), 6 substitution differences after residue 97, and 1A7 was shorter about the VDJ junction by 2 residues.
- The closest match with a full length heavy chain variable region had the following features (designation gp|U01185|MMU01185): There were 10 substitution

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differences between residues 1 and 97, [7] 6 substitutions after residue 97, and 1A7 was shorter about the VDJ junction by 3 residues.

- 1A7 differed in length from all sequences but one, due to insertions or deletions of 1 to 8 residues about the VDJ junction. For the sequence of equal length (designation pir|S11106|S11106), there were **18** substitution differences between residues 1 and 97, and [8] 7 substitutions after residue 97.
- All other comparisons showed at least **14** substitution differences between residues 1 and 97.
- All other comparisons showed at least [4] 3 substitution differences after residue 97.
- All other comparisons showed a total of at least [22] 20 insertions, deletions and substitution differences.
- Differences appeared throughout the variable region.

Amino acid consensus sequences of the 15 most closely matched V<sub>L</sub> and V<sub>H</sub> regions were designed, and compared with the 1A7 sequences. This is shown in Figure 3(C). Other than splicing differences about the VDJ junction, there appear to be about [16] 15 differences between 1A7 and the prototype sequences. Two of these differences are present in the light chain; [14] 13 are present in the heavy chain. Seven occur in the CDRs, while nine occur in the variable region framework. The point differences likely have arisen from somatic mutation of germline variable region sequences.

*In the figures N.E.*

In Figure 2, in the amino acid translation of the CDR-3 encoding sequence shown at line 20 as

"L G N Y D A L D W"

delete the letter "W" and substitute therefor -- Y --.

In Figure 3(B), delete "DWWG" in the line

"1A7: 61 SALISRLSISKDNSKSQVFLKLSLQTDATYYCAKL-----GNYDALDWWGQGTSTVTSS 117"

and substitute therefor -- DYWG --. In the following fifteen lines, delete ".Y.." and substitute therefor -- .... --.

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